

SEQUENCE LISTING

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<120> TRANSGENIC PLANTS USED AS A BIOREACTOR SYSTEM

<130> 900145.403USPC

<140> US 10/520,882

<141> 2003-07-11

<150> PCT/AU2003/000903

<151> 2003-07-11

<150> US 60/394,869

<151> 2002-07-11

<160> 56

<170> PatentIn version 3.0

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<211> 1182

<212> DNA

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Val	Ile	Lys	Ala	Ala	Leu	Glu	Arg	Ala	Gly	Val	Lys	Pro	Glu	Gln	Val	
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Ser	Glu	Val	Ile	Met	Gly	Gln	Val	Leu	Thr	Ala	Gly	Ser	Gly	Gln	Asn	
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Pro	Ala	Arg	Gln	Ala	Ala	Ile	Lys	Ala	Gly	Leu	Pro	Ala	Met	Val	Pro	
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Gly	Gly	Gln	Glu	Asn	Met	Ser	Ala	Ala	Pro	His	Val	Leu	Pro	Gly	Ser	
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Val Val Val Met Ser Ala Ala Lys Ala Lys Glu Leu Gly Leu Thr Pro	
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Lys Val Asn Val Asn Gly Gly Ala Ile Ala Ile Gly His Pro Ile Gly	
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<213> Rastonia Eutropia

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Ser Glu Val Ile Met Gly Gln Val Leu Thr Ala Gly Ser Gly Gln Asn
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Pro Ala Arg Gln Ala Ala Ile Lys Ala Gly Leu Pro Ala Met Val Pro
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Gly Gly Gln Glu Asn Met Ser Ala Ala Pro His Val Leu Pro Gly Ser
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Val Asp Gly Leu Trp Asp Val Tyr Asn Gln Tyr His Met Gly Ile Thr
 145 150 155 160

Ala Glu Asn Val Ala Lys Glu Tyr Gly Ile Thr Arg Glu Ala Gln Asp
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Glu Phe Ala Val Gly Ser Gln Asn Lys Ala Glu Ala Ala Gln Lys Ala
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 195 200 205

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Thr Leu Asp Ser Met Ser Gly Leu Lys Pro Ala Phe Asp Lys Ala Gly
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Thr Ala Ile Cys Gln Arg Leu Ala Lys Asp Gly Phe Arg Val Val Ala	
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Gly Cys Gly Pro Asn Ser Pro Arg Arg Glu Lys Trp Leu Glu Gln Gln	
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Glu Val Asp Val Leu Ile Asn Asn Ala Gly Ile Thr Arg Asp Val Val	
85 90 95	
ttc cgc aag atg acc cgc gcc gac tgg gat gcg gtg atc gac acc aac	336
Phe Arg Lys Met Thr Arg Ala Asp Trp Asp Ala Val Ile Asp Thr Asn	
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Leu Thr Ser Leu Phe Asn Val Thr Lys Gln Val Ile Asp Gly Met Ala	
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130 135 140	
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Gly	Cys	Gly	Pro	Asn	Ser	Pro	Arg	Arg	Glu	Lys	Trp	Leu	Glu	Gln	Gln		
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Lys	Ala	Leu	Gly	Phe	Asp	Phe	Ile	Ala	Ser	Glu	Gly	Asn	Val	Ala	Asp		
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115 120 125

Asp Arg Gly Trp Gly Arg Ile Val Asn Ile Ser Ser Val Asn Gly Gln
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Lys Gly Gln Phe Gly Gln Thr Asn Tyr Ser Thr Ala Lys Ala Gly Leu
145 150 155 160

His Gly Phe Thr Met Ala Leu Ala Gln Glu Val Ala Thr Lys Gly Val
165 170 175

Thr Val Asn Thr Val Ser Pro Gly Tyr Ile Ala Thr Asp Met Val Lys
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Ala Ile Arg Gln Asp Val Leu Asp Lys Ile Val Ala Thr Ile Pro Val
195 200 205

Lys Arg Leu Gly Leu Pro Glu Glu Ile Ala Ser Ile Cys Ala Trp Leu
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Gln Pro Phe Lys Val Thr Pro Gly Pro Phe Asp Pro Ala Thr Trp Leu
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gaa tgg tcc cgc cag tgg cag ggc act gaa ggc aac ggc cac gcg gcc      144
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Pro Ala Gln Leu Gly Asp Ile Gln Gln Arg Tyr Met Lys Asp Phe Ser
65      70      75      80

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Ala Leu Trp Gln Ala Met Ala Glu Gly Lys Ala Glu Ala Thr Gly Pro
      85      90      95

ctg cac gac cgg cgc ttc gcc ggc gac gca tgg cgc acc aac ctc cca      336
Leu His Asp Arg Arg Phe Ala Gly Asp Ala Trp Arg Thr Asn Leu Pro
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Tyr Arg Phe Ala Ala Ala Phe Tyr Leu Leu Asn Ala Arg Ala Leu Thr
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130      135      140

cgc ttc gcg atc tcg caa tgg gtc gat gcg atg tcg ccc gcc aac ttc      480
Arg Phe Ala Ile Ser Gln Trp Val Asp Ala Met Ser Pro Ala Asn Phe
145      150      155      160

ctt gcc acc aat ccc gag gcg cag cgc ctg ctg atc gag tcg ggc ggc      528
Leu Ala Thr Asn Pro Glu Ala Gln Arg Leu Leu Ile Glu Ser Gly Gly
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gaa tcg ctg cgt gcc ggc gtg cgc aac atg atg gaa gac ctg aca cgc      576
Glu Ser Leu Arg Ala Gly Val Arg Asn Met Met Glu Asp Leu Thr Arg
      180      185      190

ggc aag atc tcg cag acc gac gag agc gcg ttt gag gtc ggc cgc aat      624
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      195      200      205

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Glu	His	Pro	Ala	Ala	Ser	Val	Thr	Leu	Leu	Thr	Thr	Leu	Leu	Asp	Phe	
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Leu	Arg	Glu	Ala	Thr	Leu	Gly	Gly	Gly	Ala	Gly	Ala	Pro	Cys	Ala	Leu	
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Leu	Arg	Gly	Leu	Glu	Leu	Ala	Asn	Thr	Phe	Ser	Phe	Leu	Arg	Pro	Asn	
385					390					395					400	
gac	ctg	gtg	tgg	aac	tac	gtg	gtc	gac	aac	tac	ctg	aag	ggc	aac	acg	1248
Asp	Leu	Val	Trp	Asn	Tyr	Val	Val	Asp	Asn	Tyr	Leu	Lys	Gly	Asn	Thr	
				405					410					415		
ccg	gtg	ccg	ttc	gac	ctg	ctg	ttc	tgg	aac	ggc	gac	gcc	acc	aac	ctg	1296
Pro	Val	Pro	Phe	Asp	Leu	Leu	Phe	Trp	Asn	Gly	Asp	Ala	Thr	Asn	Leu	
			420					425					430			

ccg ggg ccg tgg tac tgc tgg tac ctg cgc cac acc tac ctg cag aac	1344
Pro Gly Pro Trp Tyr Cys Trp Tyr Leu Arg His Thr Tyr Leu Gln Asn	
435 440 445	
gag ctc aag gta ccg ggc aag ctg acc gtg tgc ggc gtg ccg gtg gac	1392
Glu Leu Lys Val Pro Gly Lys Leu Thr Val Cys Gly Val Pro Val Asp	
450 455 460	
ctg gcc agc atc gac gtg ccg acc tat atc tac ggc tcg cgc gaa gac	1440
Leu Ala Ser Ile Asp Val Pro Thr Tyr Ile Tyr Gly Ser Arg Glu Asp	
465 470 475 480	
cat atc gtg ccg tgg acc gcg gcc tat gcc tcg acc gcg ctg ctg gcg	1488
His Ile Val Pro Trp Thr Ala Ala Tyr Ala Ser Thr Ala Leu Leu Ala	
485 490 495	
aac aag ctg cgc ttc gtg ctg ggt gcg tcg ggc cat atc gcc ggt gtg	1536
Asn Lys Leu Arg Phe Val Leu Gly Ala Ser Gly His Ile Ala Gly Val	
500 505 510	
atc aac ccg ccg gcc aag aac aag cgc agc cac tgg act aac gat gcg	1584
Ile Asn Pro Pro Ala Lys Asn Lys Arg Ser His Trp Thr Asn Asp Ala	
515 520 525	
ctg ccg gag tcg ccg cag caa tgg ctg gcc ggc gcc atc gag cat cac	1632
Leu Pro Glu Ser Pro Gln Gln Trp Leu Ala Gly Ala Ile Glu His His	
530 535 540	
ggc agc tgg tgg ccg gac tgg acc gca tgg ctg gcc ggg cag gcc ggc	1680
Gly Ser Trp Trp Pro Asp Trp Thr Ala Trp Leu Ala Gly Gln Ala Gly	
545 550 555 560	
gcg aaa cgc gcc gcg ccc gcc aac tat ggc aat gcg cgc tat cgc gca	1728
Ala Lys Arg Ala Ala Pro Ala Asn Tyr Gly Asn Ala Arg Tyr Arg Ala	
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Ile Glu Pro Ala Pro Gly Arg Tyr Val Lys Ala Lys Ala	
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<210> 8

<211> 589

<212> PRT

<213> Rastonia Eutropia

<400> 8

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 Glu Trp Ser Arg Gln Trp Gln Gly Thr Glu Gly Asn Gly His Ala Ala
 35 40 45
 Ala Ser Gly Ile Pro Gly Leu Asp Ala Leu Ala Gly Val Lys Ile Ala
 50 55 60
 Pro Ala Gln Leu Gly Asp Ile Gln Gln Arg Tyr Met Lys Asp Phe Ser
 65 70 75 80
 Ala Leu Trp Gln Ala Met Ala Glu Gly Lys Ala Glu Ala Thr Gly Pro
 85 90 95
 Leu His Asp Arg Arg Phe Ala Gly Asp Ala Trp Arg Thr Asn Leu Pro
 100 105 110
 Tyr Arg Phe Ala Ala Ala Phe Tyr Leu Leu Asn Ala Arg Ala Leu Thr
 115 120 125
 Glu Leu Ala Asp Ala Val Glu Ala Asp Ala Lys Thr Arg Gln Arg Ile
 130 135 140
 Arg Phe Ala Ile Ser Gln Trp Val Asp Ala Met Ser Pro Ala Asn Phe
 145 150 155 160
 Leu Ala Thr Asn Pro Glu Ala Gln Arg Leu Leu Ile Glu Ser Gly Gly
 165 170 175
 Glu Ser Leu Arg Ala Gly Val Arg Asn Met Met Glu Asp Leu Thr Arg
 180 185 190
 Gly Lys Ile Ser Gln Thr Asp Glu Ser Ala Phe Glu Val Gly Arg Asn
 195 200 205
 Val Ala Val Thr Glu Gly Ala Val Val Phe Glu Asn Glu Tyr Phe Gln
 210 215 220

Leu Leu Gln Tyr Lys Pro Leu Thr Asp Lys Val His Ala Arg Pro Leu
 225 230 235 240

Leu Met Val Pro Pro Cys Ile Asn Lys Tyr Tyr Ile Leu Asp Leu Gln
 245 250 255

Pro Glu Ser Ser Leu Val Arg His Val Val Glu Gln Gly His Thr Val
 260 265 270

Phe Leu Val Ser Trp Arg Asn Pro Asp Ala Ser Met Ala Gly Ser Thr
 275 280 285

Trp Asp Asp Tyr Ile Glu His Ala Ala Ile Arg Ala Ile Glu Val Ala
 290 295 300

Arg Asp Ile Ser Gly Gln Asp Lys Ile Asn Val Leu Gly Phe Cys Val
 305 310 315 320

Gly Gly Thr Ile Val Ser Thr Ala Leu Ala Val Leu Ala Ala Arg Gly
 325 330 335

Glu His Pro Ala Ala Ser Val Thr Leu Leu Thr Thr Leu Leu Asp Phe
 340 345 350

Ala Asp Thr Gly Ile Leu Asp Val Phe Val Asp Glu Gly His Val Gln
 355 360 365

Leu Arg Glu Ala Thr Leu Gly Gly Gly Ala Gly Ala Pro Cys Ala Leu
 370 375 380

Leu Arg Gly Leu Glu Leu Ala Asn Thr Phe Ser Phe Leu Arg Pro Asn
 385 390 395 400

Asp Leu Val Trp Asn Tyr Val Val Asp Asn Tyr Leu Lys Gly Asn Thr
 405 410 415

Pro Val Pro Phe Asp Leu Leu Phe Trp Asn Gly Asp Ala Thr Asn Leu
 420 425 430

Pro Gly Pro Trp Tyr Cys Trp Tyr Leu Arg His Thr Tyr Leu Gln Asn
 435 440 445

Glu Leu Lys Val Pro Gly Lys Leu Thr Val Cys Gly Val Pro Val Asp
 450 455 460

Leu Ala Ser Ile Asp Val Pro Thr Tyr Ile Tyr Gly Ser Arg Glu Asp
 465 470 475 480

His Ile Val Pro Trp Thr Ala Ala Tyr Ala Ser Thr Ala Leu Leu Ala
 485 490 495

Asn Lys Leu Arg Phe Val Leu Gly Ala Ser Gly His Ile Ala Gly Val
 500 505 510

Ile Asn Pro Pro Ala Lys Asn Lys Arg Ser His Trp Thr Asn Asp Ala
 515 520 525

Leu Pro Glu Ser Pro Gln Gln Trp Leu Ala Gly Ala Ile Glu His His
 530 535 540

Gly Ser Trp Trp Pro Asp Trp Thr Ala Trp Leu Ala Gly Gln Ala Gly
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Ala Lys Arg Ala Ala Pro Ala Asn Tyr Gly Asn Ala Arg Tyr Arg Ala
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Ile Glu Pro Ala Pro Gly Arg Tyr Val Lys Ala Lys Ala
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<211> 1800

<212> DNA

<213> Rastonia Eutropia

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cagggcactg aaggcaacgg ccacgcggcc gcgtccggca ttccgggcct ggatgcgctg	180
gcaggcgtca agatcgcgcc ggcgagctg ggtgatatcc agcagcgcta catgaaggac	240
ttctcagcgc tgtggcaggc catggccgag ggcaaggccg aggccaccgg tccgctgcac	300
gaccggcgct tcgcccggca cgcattggcg accaacctcc catatcgctt cgctgccgcg	360
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aagaccgcc agcgcattcc cttcgcgac tcgcaatggg tcgatgcgat gtcgcccgcc	480
aacttccttg ccaccaatcc cgaggcgag cgcctgctga tcgagtcggg cggcgaatcg	540
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gagaacgagt acttcagct gttgcagtac aagccgctga ccgacaagggt gcacgcgcgc	720
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ggcgccatcg agcatcacg cagctggtgg ccggactgga ccgcatggct ggccgggcag	1680
gccggcgcg aacgcgcgc gcccgccaac tatggcaatg cgcgctatcg cgcaatcgaa	1740

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<210> 10

<211> 1428

<212> DNA

<213> Rastonia Eutropia

<220>

<221> CDS

<222> (1)..(1428)

<400> 10

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1	5	10	15	

tct agg ggg caa	tcc gcc gca atg	gct cca ttc ggc	ggc ctc aaa tcc	96
Ser Arg Gly Gln	Ser Ala Ala Met	Ala Pro Phe Gly	Gly Gly Leu Lys Ser	
20	25	30		

atg act gga ttc	cca gtg aag aag	gtc aac act gac	att act tcc att	144
Met Thr Gly Phe	Pro Val Lys Lys	Val Asn Thr Asp	Ile Thr Ser Ile	
35	40	45		

aca agc aat ggt	gga aga gta aag	tgc atg cag gtg	tgg cct cca att	192
Thr Ser Asn Gly	Gly Arg Val Lys	Cys Met Gln Val	Trp Pro Pro Ile	
50	55	60		

gga aag aag aag	ttt gag act ctt	tcc tat ttg cca	cca ttg acc aga	240
Gly Lys Lys Lys	Phe Glu Thr Leu	Ser Tyr Leu Pro	Pro Pro Leu Thr Arg	
65	70	75	80	

gat tcc cgg gtg	act gac gtt gtc	atc gta tcc gcc	gcc cgc acc gcg	288
Asp Ser Arg Val	Thr Asp Val Val	Ile Val Ser Ala	Ala Arg Thr Ala	
85	90	95		

gtc ggc aag ttt	ggc ggc tcg ctg	gcc aag atc ccg	gca ccg gaa ctg	336
Val Gly Lys Phe	Gly Gly Ser Leu	Ala Lys Ile Pro	Ala Pro Glu Leu	
100	105	110		

ggg gcc gtg gtc	atc aag gcc gcg	ctg gag cgc gcc	ggc gtc aag ccg	384
Gly Ala Val Val	Ile Lys Ala Ala	Leu Glu Arg Ala	Gly Val Lys Pro	
115	120	125		

gag	cag	gtg	agc	gaa	gtc	atc	atg	ggc	cag	gtg	ctg	acc	gcc	ggg	tcg	432
Glu	Gln	Val	Ser	Glu	Val	Ile	Met	Gly	Gln	Val	Leu	Thr	Ala	Gly	Ser	
	130					135					140					
ggc	cag	aac	ccc	gca	cgc	cag	gcc	gcg	atc	aag	gcc	ggc	ctg	ccg	gcg	480
Gly	Gln	Asn	Pro	Ala	Arg	Gln	Ala	Ala	Ile	Lys	Ala	Gly	Leu	Pro	Ala	
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atg	gtg	ccg	gcc	atg	acc	atc	aac	aag	gtg	tgc	ggc	tcg	ggc	ctg	aag	528
Met	Val	Pro	Ala	Met	Thr	Ile	Asn	Lys	Val	Cys	Gly	Ser	Gly	Leu	Lys	
				165					170					175		
gcc	gtg	atg	ctg	gcc	gcc	aac	gcg	atc	atg	gcg	ggc	gac	gcc	gag	atc	576
Ala	Val	Met	Leu	Ala	Ala	Asn	Ala	Ile	Met	Ala	Gly	Asp	Ala	Glu	Ile	
			180					185					190			
gtg	gtg	gcc	ggc	ggc	cag	gaa	aac	atg	agc	gcc	gcc	ccg	cac	gtg	ctg	624
Val	Val	Ala	Gly	Gly	Gln	Glu	Asn	Met	Ser	Ala	Ala	Pro	His	Val	Leu	
		195					200					205				
ccg	ggc	tcg	cgc	gat	ggg	ttc	cgc	atg	ggc	gat	gcc	aag	ctg	gtc	gac	672
Pro	Gly	Ser	Arg	Asp	Gly	Phe	Arg	Met	Gly	Asp	Ala	Lys	Leu	Val	Asp	
	210					215					220					
acc	atg	atc	gtc	gac	ggc	ctg	tgg	gac	gtg	tac	aac	cag	tac	cac	atg	720
Thr	Met	Ile	Val	Asp	Gly	Leu	Trp	Asp	Val	Tyr	Asn	Gln	Tyr	His	Met	
225					230					235					240	
ggc	atc	acc	gcc	gag	aac	gtg	gcc	aag	gaa	tac	ggc	atc	aca	cgc	gag	768
Gly	Ile	Thr	Ala	Glu	Asn	Val	Ala	Lys	Glu	Tyr	Gly	Ile	Thr	Arg	Glu	
				245					250					255		
gcg	cag	gat	gag	ttc	gcc	gtc	ggc	tcg	cag	aac	aag	gcc	gaa	gcc	gcg	816
Ala	Gln	Asp	Glu	Phe	Ala	Val	Gly	Ser	Gln	Asn	Lys	Ala	Glu	Ala	Ala	
			260					265					270			
cag	aag	gcc	ggc	aag	ttt	gac	gaa	gag	atc	gtc	ccg	gtg	ctg	atc	ccg	864
Gln	Lys	Ala	Gly	Lys	Phe	Asp	Glu	Glu	Ile	Val	Pro	Val	Leu	Ile	Pro	
		275					280					285				
cag	cgc	aag	ggc	gac	ccg	gtg	gcc	ttc	aag	acc	gac	gag	ttc	gtg	cgc	912
Gln	Arg	Lys	Gly	Asp	Pro	Val	Ala	Phe	Lys	Thr	Asp	Glu	Phe	Val	Arg	
	290					295					300					
cag	ggc	gcc	acg	ctg	gac	agc	atg	tcc	ggc	ctc	aag	ccc	gcc	ttc	gac	960
Gln	Gly	Ala	Thr	Leu	Asp	Ser	Met	Ser	Gly	Leu	Lys	Pro	Ala	Phe	Asp	
305					310					315					320	
aag	gcc	ggc	acg	gtg	acc	gcg	gcc	aac	gcc	tcg	ggc	ctg	aac	gac	ggc	1008
Lys	Ala	Gly	Thr	Val	Thr	Ala	Ala	Asn	Ala	Ser	Gly	Leu	Asn	Asp	Gly	
				325					330					335		
gcc	gcc	gcg	gtg	gtg	gtg	atg	tcg	gcg	gcc	aag	gcc	aag	gaa	ctg	ggc	1056

Ala	Ala	Ala	Val	Val	Val	Met	Ser	Ala	Ala	Lys	Ala	Lys	Glu	Leu	Gly		
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ctg	acc	ccg	ctg	gcc	acg	atc	aag	agc	tat	gcc	aac	gcc	ggt	gtc	gat	1104	
Leu	Thr	Pro	Leu	Ala	Thr	Ile	Lys	Ser	Tyr	Ala	Asn	Ala	Gly	Val	Asp		
		355					360					365					
ccc	aag	gtg	atg	ggc	atg	ggc	ccg	gtg	ccg	gcc	tcc	aag	cgc	gcc	ctg	1152	
Pro	Lys	Val	Met	Gly	Met	Gly	Pro	Val	Pro	Ala	Ser	Lys	Arg	Ala	Leu		
		370				375					380						
tcg	cgc	gcc	gag	tgg	acc	ccg	caa	gac	ctg	gac	ctg	atg	gag	atc	aac	1200	
Ser	Arg	Ala	Glu	Trp	Thr	Pro	Gln	Asp	Leu	Asp	Leu	Met	Glu	Ile	Asn		
385					390					395					400		
gag	gcc	ttt	gcc	gcc	cag	gcg	ctg	gcg	gtg	cac	cag	cag	atg	ggc	tgg	1248	
Glu	Ala	Phe	Ala	Ala	Gln	Ala	Leu	Ala	Val	His	Gln	Gln	Met	Gly	Trp		
			405					410						415			
gac	acc	tcc	aag	gtc	aat	gtg	aac	ggc	ggc	gcc	atc	gcc	atc	ggc	cac	1296	
Asp	Thr	Ser	Lys	Val	Asn	Val	Asn	Gly	Gly	Ala	Ile	Ala	Ile	Gly	His		
			420					425					430				
ccg	atc	ggc	gcg	tcg	ggc	tgc	cgt	atc	ctg	gtg	acg	ctg	ctg	cac	gag	1344	
Pro	Ile	Gly	Ala	Ser	Gly	Cys	Arg	Ile	Leu	Val	Thr	Leu	Leu	His	Glu		
		435					440					445					
atg	aag	cgc	cgt	gac	gcg	aag	aag	ggc	ctg	gcc	tcg	ctg	tgc	atc	ggc	1392	
Met	Lys	Arg	Arg	Asp	Ala	Lys	Lys	Gly	Leu	Ala	Ser	Leu	Cys	Ile	Gly		
		450				455					460						
ggc	ggc	atg	ggc	gtg	gcg	ctg	gca	gtc	gag	cgc	aaa					1428	
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<211> 476

<212> PRT

<213> Rastonia Eutropia

<400> 11

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		20						25					30		

Met	Thr	Gly	Phe	Pro	Val	Lys	Lys	Val	Asn	Thr	Asp	Ile	Thr	Ser	Ile	35	40	45	
Thr	Ser	Asn	Gly	Gly	Arg	Val	Lys	Cys	Met	Gln	Val	Trp	Pro	Pro	Ile	50	55	60	
Gly	Lys	Lys	Lys	Phe	Glu	Thr	Leu	Ser	Tyr	Leu	Pro	Pro	Leu	Thr	Arg	65	70	75	80
Asp	Ser	Arg	Val	Thr	Asp	Val	Val	Ile	Val	Ser	Ala	Ala	Arg	Thr	Ala	85	90	95	
Val	Gly	Lys	Phe	Gly	Gly	Ser	Leu	Ala	Lys	Ile	Pro	Ala	Pro	Glu	Leu	100	105	110	
Gly	Ala	Val	Val	Ile	Lys	Ala	Ala	Leu	Glu	Arg	Ala	Gly	Val	Lys	Pro	115	120	125	
Glu	Gln	Val	Ser	Glu	Val	Ile	Met	Gly	Gln	Val	Leu	Thr	Ala	Gly	Ser	130	135	140	
Gly	Gln	Asn	Pro	Ala	Arg	Gln	Ala	Ala	Ile	Lys	Ala	Gly	Leu	Pro	Ala	145	150	155	160
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Ala	Val	Met	Leu	Ala	Ala	Asn	Ala	Ile	Met	Ala	Gly	Asp	Ala	Glu	Ile	180	185	190	
Val	Val	Ala	Gly	Gly	Gln	Glu	Asn	Met	Ser	Ala	Ala	Pro	His	Val	Leu	195	200	205	
Pro	Gly	Ser	Arg	Asp	Gly	Phe	Arg	Met	Gly	Asp	Ala	Lys	Leu	Val	Asp	210	215	220	
Thr	Met	Ile	Val	Asp	Gly	Leu	Trp	Asp	Val	Tyr	Asn	Gln	Tyr	His	Met	225	230	235	240

Gly Ile Thr Ala Glu Asn Val Ala Lys Glu Tyr Gly Ile Thr Arg Glu
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Ala Gln Asp Glu Phe Ala Val Gly Ser Gln Asn Lys Ala Glu Ala Ala
260 265 270

Gln Lys Ala Gly Lys Phe Asp Glu Glu Ile Val Pro Val Leu Ile Pro
275 280 285

Gln Arg Lys Gly Asp Pro Val Ala Phe Lys Thr Asp Glu Phe Val Arg
290 295 300

Gln Gly Ala Thr Leu Asp Ser Met Ser Gly Leu Lys Pro Ala Phe Asp
305 310 315 320

Lys Ala Gly Thr Val Thr Ala Ala Asn Ala Ser Gly Leu Asn Asp Gly
325 330 335

Ala Ala Ala Val Val Val Met Ser Ala Ala Lys Ala Lys Glu Leu Gly
340 345 350

Leu Thr Pro Leu Ala Thr Ile Lys Ser Tyr Ala Asn Ala Gly Val Asp
355 360 365

Pro Lys Val Met Gly Met Gly Pro Val Pro Ala Ser Lys Arg Ala Leu
370 375 380

Ser Arg Ala Glu Trp Thr Pro Gln Asp Leu Asp Leu Met Glu Ile Asn
385 390 395 400

Glu Ala Phe Ala Ala Gln Ala Leu Ala Val His Gln Gln Met Gly Trp
405 410 415

Asp Thr Ser Lys Val Asn Val Asn Gly Gly Ala Ile Ala Ile Gly His
420 425 430

Pro Ile Gly Ala Ser Gly Cys Arg Ile Leu Val Thr Leu Leu His Glu
435 440 445

Met Lys Arg Arg Asp Ala Lys Lys Gly Leu Ala Ser Leu Cys Ile Gly
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<210> 12

<211> 1529

<212> DNA

<213> Rastonia Eutropia

<400> 12

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<210> 13

<211> 987

<212> DNA

<213> Rastonia Eutropia

<220>

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Ser Arg Gly Gln Ser Ala Ala Met Ala Pro Phe Gly Gly Leu Lys Ser
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atg act gga ttc cca gtg aag aag gtc aac act gac att act tcc att 144
Met Thr Gly Phe Pro Val Lys Lys Val Asn Thr Asp Ile Thr Ser Ile
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aca agc aat ggt gga aga gta aag tgc atg cag gtg tgg cct cca att 192
Thr Ser Asn Gly Gly Arg Val Lys Cys Met Gln Val Trp Pro Pro Ile
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gga aag aag aag ttt gag act ctt tcc tat ttg cca cca ttg acc aga 240
Gly Lys Lys Lys Phe Glu Thr Leu Ser Tyr Leu Pro Pro Leu Thr Arg
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gac acc aac ctg acc tcg ctg ttc aac gtc acc aag cag gtg atc gac Asp Thr Asn Leu Thr Ser Leu Phe Asn Val Thr Lys Gln Val Ile Asp 195 200 205	624
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gcc ggc ctg cat ggc ttc acc atg gca ctg gcg cag gaa gtg gcg acc Ala Gly Leu His Gly Phe Thr Met Ala Leu Ala Gln Glu Val Ala Thr 245 250 255	768
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Ile Pro Val Lys Arg Leu Gly Leu Pro Glu Glu Ile Ala Ser Ile Cys
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gcc tgg ttg tcg tcg gag gag tcc ggt ttc tcg acc ggc gcc gac ttc 960
 Ala Trp Leu Ser Ser Glu Glu Ser Gly Phe Ser Thr Gly Ala Asp Phe
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<211> 329

<212> PRT

<213> Rastonia Eutropia

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Met Thr Gly Phe Pro Val Lys Lys Val Asn Thr Asp Ile Thr Ser Ile
 35 40 45

Thr Ser Asn Gly Gly Arg Val Lys Cys Met Gln Val Trp Pro Pro Ile
 50 55 60

Gly Lys Lys Lys Phe Glu Thr Leu Ser Tyr Leu Pro Pro Leu Thr Arg
 65 70 75 80

Asp Ser Arg Val Thr Gln Arg Ile Ala Tyr Val Thr Gly Gly Met Gly
 85 90 95

Gly Ile Gly Thr Ala Ile Cys Gln Arg Leu Ala Lys Asp Gly Phe Arg
 100 105 110

Val Val Ala Gly Cys Gly Pro Asn Ser Pro Arg Arg Glu Lys Trp Leu
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Glu Gln Gln Lys Ala Leu Gly Phe Asp Phe Ile Ala Ser Glu Gly Asn
 130 135 140

Val Ala Asp Trp Asp Ser Thr Lys Thr Ala Phe Asp Lys Val Lys Ser
 145 150 155 160

Glu Val Gly Glu Val Asp Val Leu Ile Asn Asn Ala Gly Ile Thr Arg
 165 170 175

Asp Val Val Phe Arg Lys Met Thr Arg Ala Asp Trp Asp Ala Val Ile
 180 185 190

Asp Thr Asn Leu Thr Ser Leu Phe Asn Val Thr Lys Gln Val Ile Asp
 195 200 205

Gly Met Ala Asp Arg Gly Trp Gly Arg Ile Val Asn Ile Ser Ser Val
 210 215 220

Asn Gly Gln Lys Gly Gln Phe Gly Gln Thr Asn Tyr Ser Thr Ala Lys
 225 230 235 240

Ala Gly Leu His Gly Phe Thr Met Ala Leu Ala Gln Glu Val Ala Thr
 245 250 255

Lys Gly Val Thr Val Asn Thr Val Ser Pro Gly Tyr Ile Ala Thr Asp
 260 265 270

Met Val Lys Ala Ile Arg Gln Asp Val Leu Asp Lys Ile Val Ala Thr
 275 280 285

Ile Pro Val Lys Arg Leu Gly Leu Pro Glu Glu Ile Ala Ser Ile Cys
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Ser Leu Asn Gly Gly Leu His Met Gly
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<211> 1032

<212> DNA

<213> Rastonia Eutropia

<400> 15

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aagaaggtca aactgacat tacttccatt acaagcaatg gtggaagagt aaagtgcattg      180
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gagatcgctc cgatctgcgc ctggttgctg tcggaggagt ccggtttctc gaccggcgcc      960
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<212> DNA

<213> Rastonia Eutropia

<220>

<221> CDS

<222> (1)..(2016)

<400> 16

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tct	agg	ggg	caa	tcc	gcc	gca	atg	gct	cca	ttc	ggc	ggc	ctc	aaa	tcc	96
Ser	Arg	Gly	Gln	Ser	Ala	Ala	Met	Ala	Pro	Phe	Gly	Gly	Leu	Lys	Ser	
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Gly	Lys	Lys	Lys	Phe	Glu	Thr	Leu	Ser	Tyr	Leu	Pro	Pro	Leu	Thr	Arg	
65					70				75					80		

gat	tcc	cgg	gtg	gcg	acc	ggc	aaa	ggc	gcg	gca	gct	tcc	acg	cag	gaa	288
Asp	Ser	Arg	Val	Ala	Thr	Gly	Lys	Gly	Ala	Ala	Ala	Ser	Thr	Gln	Glu	
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ggc	aag	tcc	caa	cca	ttc	aag	gtc	acg	ccg	ggg	cca	ttc	gat	cca	gcc	336
Gly	Lys	Ser	Gln	Pro	Phe	Lys	Val	Thr	Pro	Gly	Pro	Phe	Asp	Pro	Ala	
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aca	tgg	ctg	gaa	tgg	tcc	cgc	cag	tgg	cag	ggc	act	gaa	ggc	aac	ggc	384
Thr	Trp	Leu	Glu	Trp	Ser	Arg	Gln	Trp	Gln	Gly	Thr	Glu	Gly	Asn	Gly	
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His	Ala	Ala	Ala	Ser	Gly	Ile	Pro	Gly	Leu	Asp	Ala	Leu	Ala	Gly	Val	
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Lys	Ile	Ala	Pro	Ala	Gln	Leu	Gly	Asp	Ile	Gln	Gln	Arg	Tyr	Met	Lys	
145					150					155				160		

gac	ttc	tca	gcg	ctg	tgg	cag	gcc	atg	gcc	gag	ggc	aag	gcc	gag	gcc	528
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Asp	Phe	Ser	Ala	Leu	Trp	Gln	Ala	Met	Ala	Glu	Gly	Lys	Ala	Glu	Ala	
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Thr	Gly	Pro	Leu	His	Asp	Arg	Arg	Phe	Ala	Gly	Asp	Ala	Trp	Arg	Thr	
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Asn	Leu	Pro	Tyr	Arg	Phe	Ala	Ala	Ala	Phe	Tyr	Leu	Leu	Asn	Ala	Arg	
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Gln	Arg	Ile	Arg	Phe	Ala	Ile	Ser	Gln	Trp	Val	Asp	Ala	Met	Ser	Pro	
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Ser	Gly	Gly	Glu	Ser	Leu	Arg	Ala	Gly	Val	Arg	Asn	Met	Met	Glu	Asp	
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Leu	Thr	Arg	Gly	Lys	Ile	Ser	Gln	Thr	Asp	Glu	Ser	Ala	Phe	Glu	Val	
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Gly	Arg	Asn	Val	Ala	Val	Thr	Glu	Gly	Ala	Val	Val	Phe	Glu	Asn	Glu	
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tac	ttc	cag	ctg	ttg	cag	tac	aag	ccg	ctg	acc	gac	aag	gtg	cac	gcg	960
Tyr	Phe	Gln	Leu	Leu	Gln	Tyr	Lys	Pro	Leu	Thr	Asp	Lys	Val	His	Ala	
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cgc	ccg	ctg	ctg	atg	gtg	ccg	ccg	tgc	atc	aac	aag	tac	tac	atc	ctg	1008
Arg	Pro	Leu	Leu	Met	Val	Pro	Pro	Cys	Ile	Asn	Lys	Tyr	Tyr	Ile	Leu	
				325					330					335		
gac	ctg	cag	ccg	gag	agc	tcg	ctg	gtg	cgc	cat	gtg	gtg	gag	cag	gga	1056
Asp	Leu	Gln	Pro	Glu	Ser	Ser	Leu	Val	Arg	His	Val	Val	Glu	Gln	Gly	
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cat	acg	gtg	ttt	ctg	gtg	tcg	tgg	cgc	aat	ccg	gac	gcc	agc	atg	gcc	1104
His	Thr	Val	Phe	Leu	Val	Ser	Trp	Arg	Asn	Pro	Asp	Ala	Ser	Met	Ala	
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ggc	agc	acc	tgg	gac	gac	tac	atc	gag	cac	gcg	gcc	atc	cgc	gcc	atc	1152
Gly	Ser	Thr	Trp	Asp	Asp	Tyr	Ile	Glu	His	Ala	Ala	Ile	Arg	Ala	Ile	
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gcg cgc ggc gag cac ccg gcc gcc agc gtc acg ctg ctg acc acg ctg Ala Arg Gly Glu His Pro Ala Ala Ser Val Thr Leu Leu Thr Thr Leu 420 425 430	1296
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cgc ccg aac gac ctg gtg tgg aac tac gtg gtc gac aac tac ctg aag Arg Pro Asn Asp Leu Val Trp Asn Tyr Val Val Asp Asn Tyr Leu Lys 485 490 495	1488
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acc aac ctg ccg ggg ccg tgg tac tgc tgg tac ctg cgc cac acc tac Thr Asn Leu Pro Gly Pro Trp Tyr Cys Trp Tyr Leu Arg His Thr Tyr 515 520 525	1584
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gcc ggt gtg atc aac ccg ccg gcc aag aac aag cgc agc cac tgg act	1824

Ala Gly Val Ile Asn Pro Pro Ala Lys Asn Lys Arg Ser His Trp Thr	
595 600 605	
aac gat gcg ctg ccg gag tcg ccg cag caa tgg ctg gcc ggc gcc atc	1872
Asn Asp Ala Leu Pro Glu Ser Pro Gln Gln Trp Leu Ala Gly Ala Ile	
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Glu His His Gly Ser Trp Trp Pro Asp Trp Thr Ala Trp Leu Ala Gly	
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Gln Ala Gly Ala Lys Arg Ala Ala Pro Ala Asn Tyr Gly Asn Ala Arg	
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Thr Trp Leu Glu Trp Ser Arg Gln Trp Gln Gly Thr Glu Gly Asn Gly
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His Ala Ala Ala Ser Gly Ile Pro Gly Leu Asp Ala Leu Ala Gly Val
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Lys Ile Ala Pro Ala Gln Leu Gly Asp Ile Gln Gln Arg Tyr Met Lys
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Asp Phe Ser Ala Leu Trp Gln Ala Met Ala Glu Gly Lys Ala Glu Ala
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Thr Gly Pro Leu His Asp Arg Arg Phe Ala Gly Asp Ala Trp Arg Thr
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Ala Asn Phe Leu Ala Thr Asn Pro Glu Ala Gln Arg Leu Leu Ile Glu
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Ser Gly Gly Glu Ser Leu Arg Ala Gly Val Arg Asn Met Met Glu Asp
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Leu Thr Arg Gly Lys Ile Ser Gln Thr Asp Glu Ser Ala Phe Glu Val
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Gly Arg Asn Val Ala Val Thr Glu Gly Ala Val Val Phe Glu Asn Glu
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Tyr Phe Gln Leu Leu Gln Tyr Lys Pro Leu Thr Asp Lys Val His Ala
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Arg Pro Leu Leu Met Val Pro Pro Cys Ile Asn Lys Tyr Tyr Ile Leu
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Asp Leu Gln Pro Glu Ser Ser Leu Val Arg His Val Val Glu Gln Gly
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His Thr Val Phe Leu Val Ser Trp Arg Asn Pro Asp Ala Ser Met Ala
355 360 365

Gly Ser Thr Trp Asp Asp Tyr Ile Glu His Ala Ala Ile Arg Ala Ile
370 375 380

Glu Val Ala Arg Asp Ile Ser Gly Gln Asp Lys Ile Asn Val Leu Gly
385 390 395 400

Phe Cys Val Gly Gly Thr Ile Val Ser Thr Ala Leu Ala Val Leu Ala
405 410 415

Ala Arg Gly Glu His Pro Ala Ala Ser Val Thr Leu Leu Thr Thr Leu
420 425 430

Leu Asp Phe Ala Asp Thr Gly Ile Leu Asp Val Phe Val Asp Glu Gly
435 440 445

His Val Gln Leu Arg Glu Ala Thr Leu Gly Gly Gly Ala Gly Ala Pro
450 455 460

Cys Ala Leu Leu Arg Gly Leu Glu Leu Ala Asn Thr Phe Ser Phe Leu
465 470 475 480

Arg Pro Asn Asp Leu Val Trp Asn Tyr Val Val Asp Asn Tyr Leu Lys
485 490 495

Gly Asn Thr Pro Val Pro Phe Asp Leu Leu Phe Trp Asn Gly Asp Ala
500 505 510

Thr Asn Leu Pro Gly Pro Trp Tyr Cys Trp Tyr Leu Arg His Thr Tyr
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Leu Gln Asn Glu Leu Lys Val Pro Gly Lys Leu Thr Val Cys Gly Val
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Pro Val Asp Leu Ala Ser Ile Asp Val Pro Thr Tyr Ile Tyr Gly Ser
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Arg Glu Asp His Ile Val Pro Trp Thr Ala Ala Tyr Ala Ser Thr Ala
 565 570 575

Leu Leu Ala Asn Lys Leu Arg Phe Val Leu Gly Ala Ser Gly His Ile
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Ala Gly Val Ile Asn Pro Pro Ala Lys Asn Lys Arg Ser His Trp Thr
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Asn Asp Ala Leu Pro Glu Ser Pro Gln Gln Trp Leu Ala Gly Ala Ile
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Glu His His Gly Ser Trp Trp Pro Asp Trp Thr Ala Trp Leu Ala Gly
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<212> DNA

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aagaaggtca aactgacat tacttccatt acaagcaatg gtggaagagt aaagtgcag 180

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<210> 19

<211> 1680

<212> DNA

<213> P. aeruginosa

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<221> CDS

<222> (1)..(1680)

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acg ctg aac ctg aat ccg gtg atc ggc atc cgg ggc aag gac ctg ctc 96
Thr Leu Asn Leu Asn Pro Val Ile Gly Ile Arg Gly Lys Asp Leu Leu
20 25 30

acc tcc gcg cgc atg gtc ctg ctc cag gcg gtg cgc cag ccg ctg cac 144
Thr Ser Ala Arg Met Val Leu Leu Gln Ala Val Arg Gln Pro Leu His
35 40 45

agc gcc agg cac gtg gcg cat ttc agc ctg gag ctg aag aac gtc ctg 192
Ser Ala Arg His Val Ala His Phe Ser Leu Glu Leu Lys Asn Val Leu
50 55 60

ctc ggc cag tcg gag cta cgc cca ggc gat gac gac cga cgc ttt tcc 240
Leu Gly Gln Ser Glu Leu Arg Pro Gly Asp Asp Asp Arg Arg Phe Ser
65 70 75 80

gat ccg gcc tgg agc cag aat cca ctg tac aag cgc tac atg cag acc 288
Asp Pro Ala Trp Ser Gln Asn Pro Leu Tyr Lys Arg Tyr Met Gln Thr
85 90 95

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Ile	Thr	Glu	Ser	Val	His	Glu	Arg	Pro	Leu	Leu	Val	Val	Pro	Pro	Gln	
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Ile	Asn	Lys	Phe	Tyr	Val	Phe	Asp	Leu	Ser	Pro	Asp	Lys	Ser	Leu	Ala	
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Asn	Pro	Thr	Lys	Ser	Gln	Arg	Glu	Trp	Gly	Leu	Thr	Thr	Tyr	Ile	Glu	
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Ala	Leu	Lys	Glu	Ala	Ile	Glu	Val	Val	Leu	Ser	Ile	Thr	Gly	Ser	Lys	
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Thr	Gln	Leu	Val	Ser	Val	Leu	Asp	Phe	Glu	Leu	Asn	Thr	Gln	Val	Ala	
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Pro	Ile	Asp	Leu	Lys	Gln	Val	Thr	Cys	Asp	Phe	Tyr	Cys	Val	Ala	Gly	
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Gln	Ser	Ile	Leu	Asn	Pro	Pro	Gly	Asn	Pro	Lys	Ala	Arg	Phe	Met	Thr	
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Asn	Pro	Glu	Leu	Pro	Ala	Glu	Pro	Lys	Ala	Trp	Leu	Glu	Gln	Ala	Gly	
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Lys	His	Ala	Asp	Ser	Trp	Trp	Leu	His	Trp	Gln	Gln	Trp	Leu	Ala	Glu	
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<212> PRT

<213> P. aeruginosa

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Thr Ser Ala Arg Met Val Leu Leu Gln Ala Val Arg Gln Pro Leu His
35 40 45

Ser Ala Arg His Val Ala His Phe Ser Leu Glu Leu Lys Asn Val Leu
50 55 60

Leu Gly Gln Ser Glu Leu Arg Pro Gly Asp Asp Asp Arg Arg Phe Ser
65 70 75 80

Asp Pro Ala Trp Ser Gln Asn Pro Leu Tyr Lys Arg Tyr Met Gln Thr
85 90 95

Tyr Leu Ala Trp Arg Lys Glu Leu His Ser Trp Ile Ser His Ser Asp
100 105 110

Leu Ser Pro Gln Asp Ile Ser Arg Gly Gln Phe Val Ile Asn Leu Leu
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Thr Glu Ala Met Ser Pro Thr Asn Ser Leu Ser Asn Pro Ala Ala Val
 130 135 140

Lys Arg Phe Phe Glu Thr Gly Gly Lys Ser Leu Leu Asp Gly Leu Gly
 145 150 155 160

His Leu Ala Lys Asp Leu Val Asn Asn Gly Gly Met Pro Ser Gln Val
 165 170 175

Asp Met Asp Ala Phe Glu Val Gly Lys Asn Leu Ala Thr Thr Glu Gly
 180 185 190

Ala Val Val Phe Arg Asn Asp Val Leu Glu Leu Ile Gln Tyr Arg Pro
 195 200 205

Ile Thr Glu Ser Val His Glu Arg Pro Leu Leu Val Val Pro Pro Gln
 210 215 220

Ile Asn Lys Phe Tyr Val Phe Asp Leu Ser Pro Asp Lys Ser Leu Ala
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Arg Phe Cys Leu Arg Asn Gly Val Gln Thr Phe Ile Val Ser Trp Arg
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Asn Pro Thr Lys Ser Gln Arg Glu Trp Gly Leu Thr Thr Tyr Ile Glu
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Ala Leu Lys Glu Ala Ile Glu Val Val Leu Ser Ile Thr Gly Ser Lys
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Leu Val Gly His Tyr Val Ala Ser Gly Glu Lys Lys Val Asn Ala Phe
 305 310 315 320

Thr Gln Leu Val Ser Val Leu Asp Phe Glu Leu Asn Thr Gln Val Ala
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Leu Phe Ala Asp Glu Lys Thr Leu Glu Ala Ala Lys Arg Arg Ser Tyr
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Gln Ser Gly Val Leu Glu Gly Lys Asp Met Ala Lys Val Phe Ala Trp
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Met Arg Pro Asn Asp Leu Ile Trp Asn Tyr Trp Val Asn Asn Tyr Leu
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Leu Gly Asn Gln Pro Pro Ala Phe Asp Ile Leu Tyr Trp Asn Asn Asp
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Thr Thr Arg Leu Pro Ala Ala Leu His Gly Glu Phe Val Glu Leu Phe
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Lys Ser Asn Pro Leu Asn Arg Pro Gly Ala Leu Glu Val Ser Gly Thr
 420 425 430

Pro Ile Asp Leu Lys Gln Val Thr Cys Asp Phe Tyr Cys Val Ala Gly
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Leu Asn Asp His Ile Thr Pro Trp Glu Ser Cys Tyr Lys Ser Ala Arg
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Leu Leu Gly Gly Lys Cys Glu Phe Ile Leu Ser Asn Ser Gly His Ile
 465 470 475 480

Gln Ser Ile Leu Asn Pro Pro Gly Asn Pro Lys Ala Arg Phe Met Thr
 485 490 495

Asn Pro Glu Leu Pro Ala Glu Pro Lys Ala Trp Leu Glu Gln Ala Gly
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Lys His Ala Asp Ser Trp Trp Leu His Trp Gln Gln Trp Leu Ala Glu
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<210> 21

<211> 1692

<212> DNA

<213> *P. aeruginosa*

<400> 21

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<400> 22

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Thr Leu Asn Leu Asn Pro Val Ile Gly Ile Arg Gly Lys Asp Leu Leu
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Thr Ser Ala Arg Met Val Leu Leu Gln Ala Val Arg Gln Pro Leu His
35 40 45

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Ser Ala Arg His Val Ala His Phe Ser Leu Glu Leu Lys Asn Val Leu
50 55 60

ctc ggc cag tcg gag cta cgc cca ggc gat gac gac cga cgc ttt tcc 240
Leu Gly Gln Ser Glu Leu Arg Pro Gly Asp Asp Arg Arg Phe Ser
65 70 75 80

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Tyr Leu Ala Trp Arg Lys Glu Leu His Ser Trp Ile Ser His Ser Asp	
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Leu Ser Pro Gln Asp Ile Ser Arg Gly Gln Phe Val Ile Asn Leu Leu	
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acc gag gcg atg tcg ccg acc aac agc ctg agc aac ccg gcg gcg gtc	432
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Ala Val Val Phe Arg Asn Asp Val Leu Glu Leu Ile Gln Tyr Arg Pro	
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Ile Thr Glu Ser Val His Glu Arg Pro Leu Leu Val Val Pro Pro Gln	
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Ile Asn Lys Phe Tyr Val Phe Asp Leu Ser Pro Asp Lys Ser Leu Ala	
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Asn Pro Thr Lys Ser Gln Arg Glu Trp Gly Leu Thr Thr Tyr Ile Glu	
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Ala Leu Lys Glu Ala Ile Glu Val Val Leu Ser Ile Thr Gly Ser Lys	
275 280 285	
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Leu	Val	Gly	His	Tyr	Val	Ala	Ser	Gly	Glu	Lys	Lys	Val	Asn	Ala	Phe	
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Thr	Gln	Leu	Val	Ser	Val	Leu	Asp	Phe	Glu	Leu	Asn	Thr	Gln	Val	Ala	
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Thr	Thr	Arg	Leu	Pro	Ala	Ala	Leu	His	Gly	Glu	Phe	Val	Glu	Leu	Phe	
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Lys	Ser	Asn	Pro	Leu	Asn	Arg	Pro	Gly	Ala	Leu	Glu	Val	Ser	Gly	Thr	
			420					425					430			
ccc	atc	gac	ctg	aag	cag	gtg	act	tgc	gac	ttc	tac	tgt	gtc	gcc	ggt	1344
Pro	Ile	Asp	Leu	Lys	Gln	Val	Thr	Cys	Asp	Phe	Tyr	Cys	Val	Ala	Gly	
		435					440					445				
ctg	aac	gac	cac	atc	acc	ccc	tgg	gag	tcg	tgc	tac	aag	tcg	gcc	agg	1392
Leu	Asn	Asp	His	Ile	Thr	Pro	Trp	Glu	Ser	Cys	Tyr	Lys	Ser	Ala	Arg	
	450					455					460					
ctg	ctg	ggt	ggc	aag	tgc	gag	ttc	atc	ctc	tcc	aac	agc	ggt	cac	atc	1440
Leu	Leu	Gly	Gly	Lys	Cys	Glu	Phe	Ile	Leu	Ser	Asn	Ser	Gly	His	Ile	
465					470					475					480	
cag	agc	atc	ctc	aac	cca	ccg	ggc	aac	ccc	aag	gca	cgc	ttc	atg	acc	1488
Gln	Ser	Ile	Leu	Asn	Pro	Pro	Gly	Asn	Pro	Lys	Ala	Arg	Phe	Met	Thr	
				485					490					495		
aat	ccg	gaa	ctg	ccc	gcc	gag	ccc	aag	gcc	tgg	ctg	gaa	cag	gcc	ggc	1536
Asn	Pro	Glu	Leu	Pro	Ala	Glu	Pro	Lys	Ala	Trp	Leu	Glu	Gln	Ala	Gly	
			500					505					510			

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Lys His Ala Asp Ser Trp Trp Leu His Trp Gln Gln Trp Leu Ala Glu
515 520 525

cgc tcc ggc aag acc cgc aag gcg ccc gcc agc ctg ggc aac aag acc 1632
Arg Ser Gly Lys Thr Arg Lys Ala Pro Ala Ser Leu Gly Asn Lys Thr
530 535 540

tat ccg gcc ggc gaa gcc gcg ccc gga acc tac gtg cat gaa cga tca 1680
Tyr Pro Ala Gly Glu Ala Ala Pro Gly Thr Tyr Val His Glu Arg Ser
545 550 555 560

aaa gct ttg ggc aaa ggt gtt acc gag gaa caa ttc aaa gag acc tgg 1728
Lys Ala Leu Gly Lys Gly Val Thr Glu Glu Gln Phe Lys Glu Thr Trp
565 570 575

acg agg ccg gga gct gct gga atg ggc gaa ggg act agc ctt gtg gtg 1776
Thr Arg Pro Gly Ala Ala Gly Met Gly Glu Gly Thr Ser Leu Val Val
580 585 590

gcc aag tcc aga atg taa 1794
Ala Lys Ser Arg Met
595

<210> 23

<211> 597

<212> PRT

<213> P. aeruginosa

<400> 23

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Thr Ser Ala Arg Met Val Leu Leu Gln Ala Val Arg Gln Pro Leu His
35 40 45

Ser Ala Arg His Val Ala His Phe Ser Leu Glu Leu Lys Asn Val Leu
50 55 60

Leu Gly Gln Ser Glu Leu Arg Pro Gly Asp Asp Asp Arg Arg Phe Ser
65 70 75 80

Asp Pro Ala Trp Ser Gln Asn Pro Leu Tyr Lys Arg Tyr Met Gln Thr
85 90 95

Tyr Leu Ala Trp Arg Lys Glu Leu His Ser Trp Ile Ser His Ser Asp
100 105 110

Leu Ser Pro Gln Asp Ile Ser Arg Gly Gln Phe Val Ile Asn Leu Leu
115 120 125

Thr Glu Ala Met Ser Pro Thr Asn Ser Leu Ser Asn Pro Ala Ala Val
130 135 140

Lys Arg Phe Phe Glu Thr Gly Gly Lys Ser Leu Leu Asp Gly Leu Gly
145 150 155 160

His Leu Ala Lys Asp Leu Val Asn Asn Gly Gly Met Pro Ser Gln Val
165 170 175

Asp Met Asp Ala Phe Glu Val Gly Lys Asn Leu Ala Thr Thr Glu Gly
180 185 190

Ala Val Val Phe Arg Asn Asp Val Leu Glu Leu Ile Gln Tyr Arg Pro
195 200 205

Ile Thr Glu Ser Val His Glu Arg Pro Leu Leu Val Val Pro Pro Gln
210 215 220

Ile Asn Lys Phe Tyr Val Phe Asp Leu Ser Pro Asp Lys Ser Leu Ala
225 230 235 240

Arg Phe Cys Leu Arg Asn Gly Val Gln Thr Phe Ile Val Ser Trp Arg
245 250 255

Asn Pro Thr Lys Ser Gln Arg Glu Trp Gly Leu Thr Thr Tyr Ile Glu
260 265 270

Ala Leu Lys Glu Ala Ile Glu Val Val Leu Ser Ile Thr Gly Ser Lys
275 280 285

Asp Leu Asn Leu Leu Gly Ala Cys Ser Gly Gly Ile Thr Thr Ala Thr
 290 295 300

Leu Val Gly His Tyr Val Ala Ser Gly Glu Lys Lys Val Asn Ala Phe
 305 310 315 320

Thr Gln Leu Val Ser Val Leu Asp Phe Glu Leu Asn Thr Gln Val Ala
 325 330 335

Leu Phe Ala Asp Glu Lys Thr Leu Glu Ala Ala Lys Arg Arg Ser Tyr
 340 345 350

Gln Ser Gly Val Leu Glu Gly Lys Asp Met Ala Lys Val Phe Ala Trp
 355 360 365

Met Arg Pro Asn Asp Leu Ile Trp Asn Tyr Trp Val Asn Asn Tyr Leu
 370 375 380

Leu Gly Asn Gln Pro Pro Ala Phe Asp Ile Leu Tyr Trp Asn Asn Asp
 385 390 395 400

Thr Thr Arg Leu Pro Ala Ala Leu His Gly Glu Phe Val Glu Leu Phe
 405 410 415

Lys Ser Asn Pro Leu Asn Arg Pro Gly Ala Leu Glu Val Ser Gly Thr
 420 425 430

Pro Ile Asp Leu Lys Gln Val Thr Cys Asp Phe Tyr Cys Val Ala Gly
 435 440 445

Leu Asn Asp His Ile Thr Pro Trp Glu Ser Cys Tyr Lys Ser Ala Arg
 450 455 460

Leu Leu Gly Gly Lys Cys Glu Phe Ile Leu Ser Asn Ser Gly His Ile
 465 470 475 480

Gln Ser Ile Leu Asn Pro Pro Gly Asn Pro Lys Ala Arg Phe Met Thr
 485 490 495

Asn Pro Glu Leu Pro Ala Glu Pro Lys Ala Trp Leu Glu Gln Ala Gly
 500 505 510

Lys His Ala Asp Ser Trp Trp Leu His Trp Gln Gln Trp Leu Ala Glu
 515 520 525

Arg Ser Gly Lys Thr Arg Lys Ala Pro Ala Ser Leu Gly Asn Lys Thr
 530 535 540

Tyr Pro Ala Gly Glu Ala Ala Pro Gly Thr Tyr Val His Glu Arg Ser
 545 550 555 560

Lys Ala Leu Gly Lys Gly Val Thr Glu Glu Gln Phe Lys Glu Thr Trp
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Thr Arg Pro Gly Ala Ala Gly Met Gly Glu Gly Thr Ser Leu Val Val
 580 585 590

Ala Lys Ser Arg Met
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<210> 24

<211> 1883

<212> DNA

<213> P. aeruginosa

<400> 24

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gcgcatggtc ctgctccagg cggatgcgcca gccgctgcac agcgccaggc acgtggcgca	180
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cgaccgacgc ttttccgatc cggcctggag ccagaatcca ctgtacaagc gctacatgca	300
gacctacctg gcctggcgca aggagctgca cagctggatc agccacagcg acctgtcgcc	360
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 gttccgcaac gacgtgctgg aactgatcca gtaccggccg atcaccgagt cgggtgcacga 660
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<210> 25

<211> 1929

<212> DNA

<213> *P. aeruginosa*

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<222> (1)..(1929)

<400> 25

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1				5					10					15		

tct	agg	ggg	caa	tcc	gcc	gca	atg	gct	cca	ttc	ggc	ggc	ctc	aaa	tcc	96
Ser	Arg	Gly	Gln	Ser	Ala	Ala	Met	Ala	Pro	Phe	Gly	Gly	Leu	Lys	Ser	
			20					25					30			

atg	act	gga	ttc	cca	gtg	aag	aag	gtc	aac	act	gac	att	act	tcc	att	144
Met	Thr	Gly	Phe	Pro	Val	Lys	Lys	Val	Asn	Thr	Asp	Ile	Thr	Ser	Ile	
		35					40					45				

aca	agc	aat	ggt	gga	aga	gta	aag	tgc	atg	cag	gtg	tgg	cct	cca	att	192
Thr	Ser	Asn	Gly	Gly	Arg	Val	Lys	Cys	Met	Gln	Val	Trp	Pro	Pro	Ile	
	50					55					60					

gga	aag	aag	aag	ttt	gag	act	ctt	tcc	tat	ttg	cca	cca	ttg	acc	aga	240
Gly	Lys	Lys	Lys	Phe	Glu	Thr	Leu	Ser	Tyr	Leu	Pro	Pro	Leu	Thr	Arg	
65				70					75					80		

gat	tcc	cgg	gtg	agt	cag	aag	aac	aat	aac	gag	ctt	ccc	aag	caa	gcc	288
Asp	Ser	Arg	Val	Ser	Gln	Lys	Asn	Asn	Asn	Glu	Leu	Pro	Lys	Gln	Ala	
			85					90						95		

gcg	gaa	aac	acg	ctg	aac	ctg	aat	ccg	gtg	atc	ggc	atc	cgg	ggc	aag	336
Ala	Glu	Asn	Thr	Leu	Asn	Leu	Asn	Pro	Val	Ile	Gly	Ile	Arg	Gly	Lys	
			100					105					110			

gac	ctg	ctc	acc	tcc	gcg	cgc	atg	gtc	ctg	ctc	cag	gcg	gtg	cgc	cag	384
Asp	Leu	Leu	Thr	Ser	Ala	Arg	Met	Val	Leu	Leu	Gln	Ala	Val	Arg	Gln	
		115					120					125				

ccg	ctg	cac	agc	gcc	agg	cac	gtg	gcg	cat	ttc	agc	ctg	gag	ctg	aag	432
Pro	Leu	His	Ser	Ala	Arg	His	Val	Ala	His	Phe	Ser	Leu	Glu	Leu	Lys	
	130					135					140					

aac	gtc	ctg	ctc	ggc	cag	tcg	gag	cta	cgc	cca	ggc	gat	gac	gac	cga	480
Asn	Val	Leu	Leu	Gly	Gln	Ser	Glu	Leu	Arg	Pro	Gly	Asp	Asp	Asp	Arg	
145					150					155					160	

cgc ttt tcc gat ccg gcc tgg agc cag aat cca ctg tac aag cgc tac	528
Arg Phe Ser Asp Pro Ala Trp Ser Gln Asn Pro Leu Tyr Lys Arg Tyr	
165 170 175	
atg cag acc tac ctg gcc tgg cgc aag gag ctg cac agc tgg atc agc	576
Met Gln Thr Tyr Leu Ala Trp Arg Lys Glu Leu His Ser Trp Ile Ser	
180 185 190	
cac agc gac ctg tcg ccg cag gac atc agt cgt ggc cag ttc gtc atc	624
His Ser Asp Leu Ser Pro Gln Asp Ile Ser Arg Gly Gln Phe Val Ile	
195 200 205	
aac ctg ctg acc gag gcg atg tcg ccg acc aac agc ctg agc aac ccg	672
Asn Leu Leu Thr Glu Ala Met Ser Pro Thr Asn Ser Leu Ser Asn Pro	
210 215 220	
gcg gcg gtc aag cgc ttc ttc gag acc ggc ggc aag agc ctg ctg gac	720
Ala Ala Val Lys Arg Phe Phe Glu Thr Gly Gly Lys Ser Leu Leu Asp	
225 230 235 240	
ggc ctc ggc cac ctg gcc aag gac ctg gtg aac aac ggc ggg atg ccg	768
Gly Leu Gly His Leu Ala Lys Asp Leu Val Asn Asn Gly Gly Met Pro	
245 250 255	
agc cag gtg gac atg gac gcc ttc gag gtg ggc aag aac ctg gcc acc	816
Ser Gln Val Asp Met Asp Ala Phe Glu Val Gly Lys Asn Leu Ala Thr	
260 265 270	
acc gag ggc gcc gtg gtg ttc cgc aac gac gtg ctg gaa ctg atc cag	864
Thr Glu Gly Ala Val Val Phe Arg Asn Asp Val Leu Glu Leu Ile Gln	
275 280 285	
tac cgg ccg atc acc gag tcg gtg cac gaa cgc ccg ctg ctg gtg gtg	912
Tyr Arg Pro Ile Thr Glu Ser Val His Glu Arg Pro Leu Leu Val Val	
290 295 300	
ccg ccg cag atc aac aag ttc tac gtc ttc gac ctg tcg ccg gac aag	960
Pro Pro Gln Ile Asn Lys Phe Tyr Val Phe Asp Leu Ser Pro Asp Lys	
305 310 315 320	
agc ctg gcg cgc ttc tgc ctg cgc aac ggc gtg cag acc ttc atc gtc	1008
Ser Leu Ala Arg Phe Cys Leu Arg Asn Gly Val Gln Thr Phe Ile Val	
325 330 335	
agt tgg cgc aac ccg acc aag tcg cag cgc gaa tgg ggc ctg acc acc	1056
Ser Trp Arg Asn Pro Thr Lys Ser Gln Arg Glu Trp Gly Leu Thr Thr	
340 345 350	
tat atc gag gcg ctc aag gag gcc atc gag gta gtc ctg tcg atc acc	1104
Tyr Ile Glu Ala Leu Lys Glu Ala Ile Glu Val Val Leu Ser Ile Thr	
355 360 365	
ggc agc aag gac ctc aac ctc ctc ggc gcc tgc tcc ggc ggg atc acc	1152

Gly 370	Ser	Lys	Asp	Leu	Asn 375	Leu	Leu	Gly	Ala	Cys 380	Ser	Gly	Gly	Ile	Thr	
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Thr 385	Ala	Thr	Leu	Val	Gly 390	His	Tyr	Val	Ala	Ser 395	Gly	Glu	Lys	Lys	Val 400	
aac	gcc	ttc	acc	caa	ctg	gtc	agc	gtg	ctc	gac	ttc	gaa	ctg	aat	acc	1248
Asn	Ala	Phe	Thr	Gln 405	Leu	Val	Ser	Val	Leu 410	Asp	Phe	Glu	Leu	Asn 415	Thr	
cag	gtc	gcg	ctg	ttc	gcc	gac	gag	aag	act	ctg	gag	gcc	gcc	aag	cgt	1296
Gln	Val	Ala	Leu 420	Phe	Ala	Asp	Glu	Lys 425	Thr	Leu	Glu	Ala	Ala 430	Lys	Arg	
cgt	tcc	tac	cag	tcc	ggc	gtg	ctg	gag	ggc	aag	gac	atg	gcc	aag	gtg	1344
Arg	Ser	Tyr 435	Gln	Ser	Gly	Val 440	Leu	Glu	Gly	Lys	Asp 445	Met	Ala	Lys	Val	
ttc	gcc	tgg	atg	cgc	ccc	aac	gac	ctg	atc	tgg	aac	tac	tgg	gtc	aac	1392
Phe 450	Ala	Trp	Met	Arg	Pro 455	Asn	Asp	Leu	Ile	Trp	Asn 460	Tyr	Trp	Val	Asn	
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Asn 465	Tyr	Leu	Leu	Gly	Asn 470	Gln	Pro	Pro	Ala	Phe 475	Asp	Ile	Leu	Tyr	Trp 480	
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Asn	Asn	Asp	Thr 485	Thr	Arg	Leu	Pro	Ala 490	Ala	Leu	His	Gly	Glu	Phe 495	Val	
gaa	ctg	ttc	aag	agc	aac	ccg	ctg	aac	cgc	ccc	ggc	gcc	ctg	gag	gtc	1536
Glu	Leu	Phe 500	Lys	Ser	Asn	Pro	Leu 505	Asn	Arg	Pro	Gly	Ala 510	Leu	Glu	Val	
tcc	ggc	acg	ccc	atc	gac	ctg	aag	cag	gtg	act	tgc	gac	ttc	tac	tgt	1584
Ser	Gly 515	Thr	Pro	Ile	Asp	Leu 520	Lys	Gln	Val	Thr	Cys 525	Asp	Phe	Tyr	Cys	
gtc	gcc	ggt	ctg	aac	gac	cac	atc	acc	ccc	tgg	gag	tcg	tgc	tac	aag	1632
Val 530	Ala	Gly	Leu	Asn	Asp	His 535	Ile	Thr	Pro	Trp	Glu 540	Ser	Cys	Tyr	Lys	
tcg	gcc	agg	ctg	ctg	ggt	ggc	aag	tgc	gag	ttc	atc	ctc	tcc	aac	agc	1680
Ser 545	Ala	Arg	Leu	Leu	Gly 550	Gly	Lys	Cys	Glu	Phe 555	Ile	Leu	Ser	Asn 560	Ser	
ggt	cac	atc	cag	agc	atc	ctc	aac	cca	ccg	ggc	aac	ccc	aag	gca	cgc	1728
Gly	His	Ile	Gln	Ser 565	Ile	Leu	Asn	Pro	Pro 570	Gly	Asn	Pro	Lys	Ala 575	Arg	
ttc	atg	acc	aat	ccg	gaa	ctg	ccc	gcc	gag	ccc	aag	gcc	tgg	ctg	gaa	1776
Phe	Met	Thr 580	Asn	Pro	Glu	Leu	Pro 585	Ala	Glu	Pro	Lys	Ala 590	Trp	Leu	Glu	

cag gcc ggc aag cac gcc gac tcg tgg tgg ttg cac tgg cag caa tgg 1824
Gln Ala Gly Lys His Ala Asp Ser Trp Trp Leu His Trp Gln Gln Trp
595 600 605

ctg gcc gaa cgc tcc ggc aag acc cgc aag gcg ccc gcc agc ctg ggc 1872
Leu Ala Glu Arg Ser Gly Lys Thr Arg Lys Ala Pro Ala Ser Leu Gly
610 615 620

aac aag acc tat ccg gcc ggc gaa gcc gcg ccc gga acc tac gtg cat 1920
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625 630 635 640

gaa cga tga	1929
Glu Arg	

<210> 26

<211> 642

<212> PRT

<213> P. aeruginosa

<400> 26

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35 40 45

Thr Ser Asn Gly Gly Arg Val Lys Cys Met Gln Val Trp Pro Pro Ile
50 55 60

Gly Lys Lys Lys Phe Glu Thr Leu Ser Tyr Leu Pro Pro Leu Thr Arg
65 70 75 80

Asp Ser Arg Val Ser Gln Lys Asn Asn Asn Glu Leu Pro Lys Gln Ala
85 90 95

Ala Glu Asn Thr Leu Asn Leu Asn Pro Val Ile Gly Ile Arg Gly Lys
 100 105 110

Asp Leu Leu Thr Ser Ala Arg Met Val Leu Leu Gln Ala Val Arg Gln
 115 120 125

Pro Leu His Ser Ala Arg His Val Ala His Phe Ser Leu Glu Leu Lys
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Asn Val Leu Leu Gly Gln Ser Glu Leu Arg Pro Gly Asp Asp Asp Arg
 145 150 155 160

Arg Phe Ser Asp Pro Ala Trp Ser Gln Asn Pro Leu Tyr Lys Arg Tyr
 165 170 175

Met Gln Thr Tyr Leu Ala Trp Arg Lys Glu Leu His Ser Trp Ile Ser
 180 185 190

His Ser Asp Leu Ser Pro Gln Asp Ile Ser Arg Gly Gln Phe Val Ile
 195 200 205

Asn Leu Leu Thr Glu Ala Met Ser Pro Thr Asn Ser Leu Ser Asn Pro
 210 215 220

Ala Ala Val Lys Arg Phe Phe Glu Thr Gly Gly Lys Ser Leu Leu Asp
 225 230 235 240

Gly Leu Gly His Leu Ala Lys Asp Leu Val Asn Asn Gly Gly Met Pro
 245 250 255

Ser Gln Val Asp Met Asp Ala Phe Glu Val Gly Lys Asn Leu Ala Thr
 260 265 270

Thr Glu Gly Ala Val Val Phe Arg Asn Asp Val Leu Glu Leu Ile Gln
 275 280 285

Tyr Arg Pro Ile Thr Glu Ser Val His Glu Arg Pro Leu Leu Val Val
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Pro Pro Gln Ile Asn Lys Phe Tyr Val Phe Asp Leu Ser Pro Asp Lys
 305 310 315 320

Ser Leu Ala Arg Phe Cys Leu Arg Asn Gly Val Gln Thr Phe Ile Val
 325 330 335

Ser Trp Arg Asn Pro Thr Lys Ser Gln Arg Glu Trp Gly Leu Thr Thr
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Tyr Ile Glu Ala Leu Lys Glu Ala Ile Glu Val Val Leu Ser Ile Thr
 355 360 365

Gly Ser Lys Asp Leu Asn Leu Leu Gly Ala Cys Ser Gly Gly Ile Thr
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Thr Ala Thr Leu Val Gly His Tyr Val Ala Ser Gly Glu Lys Lys Val
 385 390 395 400

Asn Ala Phe Thr Gln Leu Val Ser Val Leu Asp Phe Glu Leu Asn Thr
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Gln Val Ala Leu Phe Ala Asp Glu Lys Thr Leu Glu Ala Ala Lys Arg
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Arg Ser Tyr Gln Ser Gly Val Leu Glu Gly Lys Asp Met Ala Lys Val
 435 440 445

Phe Ala Trp Met Arg Pro Asn Asp Leu Ile Trp Asn Tyr Trp Val Asn
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Asn Tyr Leu Leu Gly Asn Gln Pro Pro Ala Phe Asp Ile Leu Tyr Trp
 465 470 475 480

Asn Asn Asp Thr Thr Arg Leu Pro Ala Ala Leu His Gly Glu Phe Val
 485 490 495

Glu Leu Phe Lys Ser Asn Pro Leu Asn Arg Pro Gly Ala Leu Glu Val
 500 505 510

Ser Gly Thr Pro Ile Asp Leu Lys Gln Val Thr Cys Asp Phe Tyr Cys
 515 520 525

Val Ala Gly Leu Asn Asp His Ile Thr Pro Trp Glu Ser Cys Tyr Lys
 530 535 540

Ser Ala Arg Leu Leu Gly Gly Lys Cys Glu Phe Ile Leu Ser Asn Ser
 545 550 555 560

Gly His Ile Gln Ser Ile Leu Asn Pro Pro Gly Asn Pro Lys Ala Arg
 565 570 575

Phe Met Thr Asn Pro Glu Leu Pro Ala Glu Pro Lys Ala Trp Leu Glu
 580 585 590

Gln Ala Gly Lys His Ala Asp Ser Trp Trp Leu His Trp Gln Gln Trp
 595 600 605

Leu Ala Glu Arg Ser Gly Lys Thr Arg Lys Ala Pro Ala Ser Leu Gly
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Asn Lys Thr Tyr Pro Ala Gly Glu Ala Ala Pro Gly Thr Tyr Val His
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Glu Arg

<210> 27

<211> 1941

<212> DNA

<213> *P. aeruginosa*

<400> 27

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aacagcctga	gcaacccggc	ggcgggtcaag	cgcttcttcg	agaccggcgg	caagagcctg	720
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cgcccgtgctgc	tggtggtgcc	gccgcagatc	aacaagttct	acgtcttcga	cctgtcgccg	960
gacaagagcc	tggcgcgctt	ctgcctgcgc	aacggcgtgc	agaccttcac	cgtcagttgg	1020
cgcaaccgca	ccaagtgcga	gcgcgaatgg	ggcctgacca	cctatatcga	ggcgctcaag	1080
gaggccatcg	aggtagtctt	gtcgatcacc	ggcagcaagg	acctcaacct	cctcggcgcc	1140
tgctccggcg	ggatcaccac	cgcgaccctg	gtcggccact	acgtggccag	cggcgagaag	1200
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gcgctgttcg	ccgacgagaa	gactctggag	gccgccaagc	gtcgttcta	ccagtccggc	1320
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aacagcggtc	acatccagag	catcctcaac	ccaccgggca	acccaaggc	acgcttcacg	1740
accaatccgg	aactgcccgc	cgagcccaag	gcctggctgg	aacaggccgg	caagcacgcc	1800
gactcgtggt	ggttgactg	gcagcaatgg	ctggccgaac	gctccggcaa	gacccgcaag	1860
gcgcccgcga	gcctgggcaa	caagacctat	ccggccggcg	aagccgcgcc	cggaacctac	1920
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<210> 28

<211> 1137

<212> DNA

<213> *Pseudomonas putida*

<220>

<221> CDS

<222> (1)..(1137)

<400> 28

atg gct tct atg ata tcc tct tcc gct gtg aca aca gtc agc cgt gcc	48
Met Ala Ser Met Ile Ser Ser Ser Ala Val Thr Thr Val Ser Arg Ala	
1 5 10 15	

tct agg ggg caa tcc gcc gca atg gct cca ttc ggc ggc ctc aaa tcc	96
Ser Arg Gly Gln Ser Ala Ala Met Ala Pro Phe Gly Gly Leu Lys Ser	
20 25 30	

atg act gga ttc cca gtg aag aag gtc aac act gac att act tcc att	144
Met Thr Gly Phe Pro Val Lys Lys Val Asn Thr Asp Ile Thr Ser Ile	
35 40 45	

aca agc aat ggt gga aga gta aag tgc atg cag gtg tgg cct cca att	192
Thr Ser Asn Gly Gly Arg Val Lys Cys Met Gln Val Trp Pro Pro Ile	
50 55 60	

gga aag aag aag ttt gag act ctt tcc tat ttg cca cca ttg acc aga	240
Gly Lys Lys Lys Phe Glu Thr Leu Ser Tyr Leu Pro Pro Leu Thr Arg	
65 70 75 80	

gat tcc cgg gtg agg cca gaa atc gct gta ctt gat atc caa ggt cag	288
Asp Ser Arg Val Arg Pro Glu Ile Ala Val Leu Asp Ile Gln Gly Gln	
85 90 95	

tat cgg gtt tac acg gag ttc tat cgc gcg gat gcg gcc gaa aac acg	336
Tyr Arg Val Tyr Thr Glu Phe Tyr Arg Ala Asp Ala Ala Glu Asn Thr	
100 105 110	

atc atc ctg atc aac ggc tcg ctg gcc acc acg gcc tcg ttc gcc cag	384
Ile Ile Leu Ile Asn Gly Ser Leu Ala Thr Thr Ala Ser Phe Ala Gln	
115 120 125	

acg gta cgt aac ctg cac cca cag ttc aac gtg gtt ctg ttc gac cag	432
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Thr	Val	Arg	Asn	Leu	His	Pro	Gln	Phe	Asn	Val	Val	Leu	Phe	Asp	Gln	
130						135					140					
ccg	tat	tca	ggc	aag	tcc	aag	ccg	cac	aac	cgt	cag	gaa	cgg	ctg	atc	480
Pro	Tyr	Ser	Gly	Lys	Ser	Lys	Pro	His	Asn	Arg	Gln	Glu	Arg	Leu	Ile	
145					150					155					160	
agc	aag	gag	acc	gag	gcg	cat	atc	ctc	ctt	gag	ctg	atc	gag	cac	ttc	528
Ser	Lys	Glu	Thr	Glu	Ala	His	Ile	Leu	Leu	Glu	Leu	Ile	Glu	His	Phe	
				165					170					175		
cag	gca	gac	cac	gtg	atg	tct	ttt	tcg	tgg	ggc	ggc	gca	agc	acg	ctg	576
Gln	Ala	Asp	His	Val	Met	Ser	Phe	Ser	Trp	Gly	Gly	Ala	Ser	Thr	Leu	
			180					185					190			
ctg	gcg	ctg	gcg	cac	cag	ccg	cgg	tac	gtg	aag	aag	gca	gtg	gtg	agt	624
Leu	Ala	Leu	Ala	His	Gln	Pro	Arg	Tyr	Val	Lys	Lys	Ala	Val	Val	Ser	
		195					200					205				
tcg	ttc	tcg	cca	gtg	atc	aac	gag	ccg	atg	cgc	gac	tat	ctg	gac	cgt	672
Ser	Phe	Ser	Pro	Val	Ile	Asn	Glu	Pro	Met	Arg	Asp	Tyr	Leu	Asp	Arg	
	210					215					220					
ggc	tgc	cag	tac	ctg	gcc	gcc	tgc	gac	cgt	tat	cag	gtc	ggc	aac	ctg	720
Gly	Cys	Gln	Tyr	Leu	Ala	Ala	Cys	Asp	Arg	Tyr	Gln	Val	Gly	Asn	Leu	
225					230					235					240	
gtc	aat	gac	acc	atc	ggc	aag	cac	ttg	ccg	tcg	ctg	ttc	aaa	cgc	ttc	768
Val	Asn	Asp	Thr	Ile	Gly	Lys	His	Leu	Pro	Ser	Leu	Phe	Lys	Arg	Phe	
				245					250					255		
aac	tac	cgc	cat	gtg	agc	agc	ctg	gac	agc	cac	gag	tac	gca	cag	atg	816
Asn	Tyr	Arg	His	Val	Ser	Ser	Leu	Asp	Ser	His	Glu	Tyr	Ala	Gln	Met	
			260					265					270			
cac	ttc	cac	atc	aac	cag	gtg	ctg	gag	cac	gac	ctg	gaa	cgt	gcg	ctg	864
His	Phe	His	Ile	Asn	Gln	Val	Leu	Glu	His	Asp	Leu	Glu	Arg	Ala	Leu	
		275					280					285				
caa	ggc	gcg	cgc	aat	atc	aac	atc	ccg	gtg	ctg	ttc	atc	aac	ggc	gag	912
Gln	Gly	Ala	Arg	Asn	Ile	Asn	Ile	Pro	Val	Leu	Phe	Ile	Asn	Gly	Glu	
	290					295					300					
cgc	gac	gag	tac	acc	aca	gtc	gag	gat	gcg	cgg	cag	ttc	agc	aag	cat	960
Arg	Asp	Glu	Tyr	Thr	Thr	Val	Glu	Asp	Ala	Arg	Gln	Phe	Ser	Lys	His	
305					310					315					320	
gtg	ggc	aga	agc	cag	ttc	agc	gtg	atc	cgc	gat	gcg	ggc	cac	ttc	ctg	1008
Val	Gly	Arg	Ser	Gln	Phe	Ser	Val	Ile	Arg	Asp	Ala	Gly	His	Phe	Leu	
				325					330				335			
gac	atg	gag	aac	aag	acc	gcc	tgc	gag	aac	acc	cgc	aat	gtc	atg	ctg	1056
Asp	Met	Glu	Asn	Lys	Thr	Ala	Cys	Glu	Asn	Thr	Arg	Asn	Val	Met	Leu	
			340					345					350			

ggc ttc ctc aag cca acc gtg cgt gaa ccc cgc caa cgt tac caa ccc 1104
Gly Phe Leu Lys Pro Thr Val Arg Glu Pro Arg Gln Arg Tyr Gln Pro
355 360 365

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gtg cag cag ggg cag cat gca ttt gcc atc tga      1137
Val Gln Gln Gly Gln His Ala Phe Ala Ile
      370              375
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<210> 29

<211> 378

<212> PRT

<213> Pseudomonas putida

<400> 29

Met Ala Ser Met Ile Ser Ser Ser Ala Val Thr Thr Val Ser Arg Ala
1 5 10 15

Ser Arg Gly Gln Ser Ala Ala Met Ala Pro Phe Gly Gly Leu Lys Ser
20 25 30

Met Thr Gly Phe Pro Val Lys Lys Val Asn Thr Asp Ile Thr Ser Ile
35 40 45

Thr Ser Asn Gly Gly Arg Val Lys Cys Met Gln Val Trp Pro Pro Ile
50 55 60

Gly Lys Lys Lys Phe Glu Thr Leu Ser Tyr Leu Pro Pro Leu Thr Arg
65 70 75 80

Asp Ser Arg Val Arg Pro Glu Ile Ala Val Leu Asp Ile Gln Gly Gln
85 90 95

Tyr Arg Val Tyr Thr Glu Phe Tyr Arg Ala Asp Ala Ala Glu Asn Thr
100 105 110

Ile Ile Leu Ile Asn Gly Ser Leu Ala Thr Thr Ala Ser Phe Ala Gln
115 120 125

Thr Val Arg Asn Leu His Pro Gln Phe Asn Val Val Leu Phe Asp Gln
 130 135 140

Pro Tyr Ser Gly Lys Ser Lys Pro His Asn Arg Gln Glu Arg Leu Ile
 145 150 155 160

Ser Lys Glu Thr Glu Ala His Ile Leu Leu Glu Leu Ile Glu His Phe
 165 170 175

Gln Ala Asp His Val Met Ser Phe Ser Trp Gly Gly Ala Ser Thr Leu
 180 185 190

Leu Ala Leu Ala His Gln Pro Arg Tyr Val Lys Lys Ala Val Val Ser
 195 200 205

Ser Phe Ser Pro Val Ile Asn Glu Pro Met Arg Asp Tyr Leu Asp Arg
 210 215 220

Gly Cys Gln Tyr Leu Ala Ala Cys Asp Arg Tyr Gln Val Gly Asn Leu
 225 230 235 240

Val Asn Asp Thr Ile Gly Lys His Leu Pro Ser Leu Phe Lys Arg Phe
 245 250 255

Asn Tyr Arg His Val Ser Ser Leu Asp Ser His Glu Tyr Ala Gln Met
 260 265 270

His Phe His Ile Asn Gln Val Leu Glu His Asp Leu Glu Arg Ala Leu
 275 280 285

Gln Gly Ala Arg Asn Ile Asn Ile Pro Val Leu Phe Ile Asn Gly Glu
 290 295 300

Arg Asp Glu Tyr Thr Thr Val Glu Asp Ala Arg Gln Phe Ser Lys His
 305 310 315 320

Val Gly Arg Ser Gln Phe Ser Val Ile Arg Asp Ala Gly His Phe Leu
 325 330 335

Asp Met Glu Asn Lys Thr Ala Cys Glu Asn Thr Arg Asn Val Met Leu
 340 345 350

Gly Phe Leu Lys Pro Thr Val Arg Glu Pro Arg Gln Arg Tyr Gln Pro
 355 360 365

Val Gln Gln Gly Gln His Ala Phe Ala Ile
 370 375

<210> 30

<211> 1149

<212> DNA

<213> *Pseudomonas putida*

<400> 30

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gggcaatccg ccgcaatggc tccattcggc ggcctcaaatt ccatgactgg attcccagtg      120
aagaagggtca acactgacat tactttccatt acaagcaatg gtggaagagt aaagtgcattg      180
cagggtgtggc ctccaattgg aaagaagaag tttgagactc tttcctatatt gccaccattg      240
accagagatt cccgggtgag gccagaaatc gctgtacttg atatccaagg tcagtatcgg      300
gtttacacgg agttctatcg cgcggatgcg gccgaaaaca cgatcatcct gatcaacggc      360
tcgctggcca ccacggcctc gttcgcccag acggtacgta acctgcaccc acagttcaac      420
gtggttctgt tcgaccagcc gtattcaggc aagtccaagc cgacaaccg tcaggaacgg      480
ctgatcagca aggagaccga ggcgcataatc ctctttgagc tgatcgagca cttccaggca      540
gaccacgtga tgtctttttc gtgggggtggc gcaagcacgc tgctggcgct ggcgaccag      600
ccgcggtacg tgaagaaggc agtgggtgagt tcgtttctcgc cagtgatcaa cgagccgatg      660
cgcgactatc tggaccgtgg ctgccagtac ctggccgcct gcgaccgtta tcaggtcggc      720
aacctgggtca atgacaccat cggcaagcac ttgccgtcgc tgttcaaacg cttcaactac      780
cgccatgtga gcagcctgga cagccacgag tacgcacaga tgcacttcca catcaaccag      840
gtgctggagc acgacctgga acgtgcgctg caaggcgcgc gcaatatcaa catcccgggtg      900
ctgttcatca acggcgagcg cgacgagtag accacagtcg aggatgcgcg gcagttcagc      960
aagcatgtgg gcagaagcca gttcagcgtg atccgcgatg cgggccactt cctggacatg     1020

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gagaacaaga ccgcctgcga gaacacccgc aatgtcatgc tgggcttcct caagccaacc 1080
 gtgcgtgaac cccgccaacg ttaccaaccc gtgcagcagg ggcagcatgc atttgccatc 1140
 tgaggtacc 1149

<210> 31

<211> 519

<212> DNA

<213> *Aeromonas caviae*

<220>

<221> CDS

<222> (1)..(519)

<400> 31

atg agc gca caa tcc ctg gaa gta ggc cag aag gcc cgt ctc agc aag 48
 Met Ser Ala Gln Ser Leu Glu Val Gly Gln Lys Ala Arg Leu Ser Lys
 1 5 10 15

cgg ttc ggg gcg gcg gag gta gcc gcc ttc gcc gcg ctc tcg gag gac 96
 Arg Phe Gly Ala Ala Glu Val Ala Ala Phe Ala Ala Leu Ser Glu Asp
 20 25 30

ttc aac ccc ctg cac ctg gac ccg gcc ttc gcc gcc acc acg gcg ttc 144
 Phe Asn Pro Leu His Leu Asp Pro Ala Phe Ala Ala Thr Thr Ala Phe
 35 40 45

gag cgg ccc ata gtc cac ggc atg ctg ctc gcc agc ctc ttc tcc ggg 192
 Glu Arg Pro Ile Val His Gly Met Leu Leu Ala Ser Leu Phe Ser Gly
 50 55 60

ctg ctg ggc cag cag ttg ccg ggc aag ggg agc atc tat ctg ggt caa 240
 Leu Leu Gly Gln Gln Leu Pro Gly Lys Gly Ser Ile Tyr Leu Gly Gln
 65 70 75 80

agc ctc agc ttc aag ctg ccg gtc ttt gtc ggg gac gag gtg acg gcc 288
 Ser Leu Ser Phe Lys Leu Pro Val Phe Val Gly Asp Glu Val Thr Ala
 85 90 95

gag gtg gag gtg acc gcc ctt cgc gag gac aag ccc atc gcc acc ctg 336
 Glu Val Glu Val Thr Ala Leu Arg Glu Asp Lys Pro Ile Ala Thr Leu
 100 105 110

acc acc cgc atc ttc acc caa ggc ggc gcc ctg gcc gtg acg ggg gaa 384
 Thr Thr Arg Ile Phe Thr Gln Gly Gly Ala Leu Ala Val Thr Gly Glu
 115 120 125

gcc gtg gtc aag ctg cct tca aaa gct ttg ggc aaa ggt gtt acc gag 432
 Ala Val Val Lys Leu Pro Ser Lys Ala Leu Gly Lys Gly Val Thr Glu
 130 135 140

gaa caa ttc aaa gag acc tgg acg agg ccg gga gct gct gga atg ggc 480
 Glu Gln Phe Lys Glu Thr Trp Thr Arg Pro Gly Ala Ala Gly Met Gly
 145 150 155 160

gaa ggg act agc ctt gtg gtg gcc aag tcc aga atg taa 519
 Glu Gly Thr Ser Leu Val Val Ala Lys Ser Arg Met
 165 170

<210> 32

<211> 172

<212> PRT

<213> *Aeromonas caviae*

<400> 32

Met Ser Ala Gln Ser Leu Glu Val Gly Gln Lys Ala Arg Leu Ser Lys
 1 5 10 15

Arg Phe Gly Ala Ala Glu Val Ala Ala Phe Ala Ala Leu Ser Glu Asp
 20 25 30

Phe Asn Pro Leu His Leu Asp Pro Ala Phe Ala Ala Thr Thr Ala Phe
 35 40 45

Glu Arg Pro Ile Val His Gly Met Leu Leu Ala Ser Leu Phe Ser Gly
 50 55 60

Leu Leu Gly Gln Gln Leu Pro Gly Lys Gly Ser Ile Tyr Leu Gly Gln
 65 70 75 80

Ser Leu Ser Phe Lys Leu Pro Val Phe Val Gly Asp Glu Val Thr Ala
 85 90 95

Glu Val Glu Val Thr Ala Leu Arg Glu Asp Lys Pro Ile Ala Thr Leu
 100 105 110

Thr Thr Arg Ile Phe Thr Gln Gly Gly Ala Leu Ala Val Thr Gly Glu
 115 120 125

Ala Val Val Lys Leu Pro Ser Lys Ala Leu Gly Lys Gly Val Thr Glu
 130 135 140

Glu Gln Phe Lys Glu Thr Trp Thr Arg Pro Gly Ala Ala Gly Met Gly
 145 150 155 160

Glu Gly Thr Ser Leu Val Val Ala Lys Ser Arg Met
 165 170

<210> 33

<211> 598

<212> DNA

<213> *Aeromonas caviae*

<400> 33

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ggatccatga gcgcacaatc cctggaagta ggccagaagg cccgtctcag caagcggttc      60
ggggcggcgg aggtagccgc cttcgccgcg ctctcgaggg acttcaaccc cctgcacctg    120
gacccggcct tcgccgccac cacggcggtt gagcggccca tagtccacgg catgctgctc    180
gccagcctct tctccggggt gctggggccag cagttgccgg gcaaggggag catctatctg    240
ggtcaaagcc tcagcttcaa gctgccggtc tttgtcgggg acgaggtgac ggccgaggtg    300
gaggtgaccg cccttcgcga ggacaagccc atcgccaccc tgaccaccg catcttcacc    360
caaggcggcg ccctcgccgt gacgggggaa gccgtgggtca agctgccttc aaaagctttg    420
ggcaaaggtg ttaccgagga acaattcaaa gagacctgga cgaggccggg agctgctgga    480
atgggcgaag ggcgaaggga ctagccttgt ggtggccaag tccagaatgt aagacagacg    540
ttcattgcgg cggagcggcc aaggcgggtt ggcattcttc cagaaaaaca actagggg      598

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<210> 34

<211> 31

<212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer TphaF

<221> misc_feature
 <222> 1, 2, 3, 4, 5, 6
 <223> n = A,T,C or G

<400> 34
 nnnnnnggat ccatggcttc tatgatatcc t 31

<210> 35
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer PhaF

<221> misc_feature
 <222> 1, 2, 3, 4, 5, 6
 <223> n = A,T,C or G

<400> 35
 nnnnnnggat ccatgactga cgttgatcatc 30

<210> 36
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer PhbF

<221> misc_feature
 <222> 1, 2, 3, 4, 5, 6
 <223> n = A,T,C or G

<400> 36
 nnnnnnggat ccatgactca gcgcattgac 30

<210> 37
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer PhcF

<221> misc_feature
 <222> 1, 2, 3, 4, 5, 6

<223> n = A,T,C or G

<400> 37
nnnnnnggat ccatggcgac cggcaaaggc 30

<210> 38
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer PhaR

<400> 38
ctgagtcatg tccactcc 18

<210> 39
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer PhbR

<400> 39
ctgccgactg gtggaacc 18

<210> 40
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer PhcR

<400> 40
gaagcgtcat gccttggc 18

<210> 41
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer PhaClCf

<221> misc_feature
<222> 1, 2, 3, 4, 5, 6
<223> n = A,T,C or G

<400> 41
nnnnnnggat ccatgagcca gaagaac 27

<210> 42

<211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer PhaC1Cr

<221> misc_feature
 <222> 1, 2, 3, 4, 5, 6
 <223> n = A,T,C or G

<400> 42
 nnnnnnggta cctcatcggt catgcacg

28

<210> 43
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer PhaC1Pf

<221> misc_feature
 <222> 1, 2, 3, 4, 5, 6
 <223> n = A,T,C or G

<400> 43
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32

<210> 44
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer PhaJF

<400> 44
 ggatccatga gcgcacaatc cctgg

25

<210> 45
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer PhaJR

<400> 45
 aagcttttga aggcagcttg accacgg

27

<210> 46
 <211> 27
 <212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer PhaGF

<400> 46

cccgggtgag gccagaaatc gctgtac

27

<210> 47

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer PhaGR

<400> 47

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25

<210> 48

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer SSP-F

<221> misc_feature

<222> 1, 2

<223> n = A,T,C or G

<400> 48

nngagctcga tgggaggtgc tcgaagacat attacc

36

<210> 49

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer SSP-R

<221> misc_feature

<222> 1, 2

<223> n = A,T,C or G

<400> 49

nnggatcctg tactagatat ggcagc

26

<210> 50

<211> 38

<212> DNA

<213> Artificial Sequence

<220>
 <223> PCR primer 3

 <400> 50
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 <210> 51
 <211> 35
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> PCR primer 4

 <400> 51
 catcttactg gtaccttttag tacaacggtg acgcc 35

 <210> 52
 <211> 39
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> PCR primer 5

 <400> 52
 ctactcattt actagtcacc atgagcacat acgaaggtc 39

 <210> 53
 <211> 36
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> PCR primer 6

 <400> 53
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 <210> 54
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> PCR primer 1

 <400> 54
 ctactcataa ccatggcgcc caccgtg 27

 <210> 55
 <211> 43
 <212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer 2

<400> 55

catcttactc atatgccgca cctgcatgca ccggatcctt ccg

43

<210> 56

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Five extra N-terminal amino acid residues in a CPL
variant

<400> 56

Met Gln Val Arg His

1

5